SDS at 37°C, followed by one wash for 20 minutes in 0.2X SSC at a temperature of about 50°C.

REMARKS

1. Status of the Claims

In this Amendment, claims 4, 11, and 14 are canceled, claims 1, 2, 9 and 15 are amended and claims 25-28 are added. Therefore claims 1-2, 5-10, 12-13, 15, and 17-29 are pending and under consideration with entry of this Amendment.

A marked up copy of amended claims 1, 2, 9 and 15 is provided as appendix A entitled "**MARKED UP COPY OF CLAIMS**." As a convenience to the Examiner, a complete set of the claims, as amended herein, is also attached to this Amendment as Appendix B.

2. Support for the Amendments

Support for the amendments to the claims can be found throughout the specification, the drawings, and the claims as originally drafted. For example, support for WD40 repeats can be found on, e.g., page 4, lines 12-15 of the specification. Support for the hybridization conditions recited in new claim 29 can be found on, e.g., page 10, lines 3-7 of the present application. No new matter is introduced by this Amendment.

3. Cross-Reference to related applications

The Examiner noted that the cross-reference to related applications section of the patent application required updating. The appropriate paragraph is amended.

4. Objections to the specification

A. Hyperlink

The Examiner objected to the specification because it contains hyperlinks. Specifically, the Examiner noted that the specification contains a hyperlink at page 7, line 5 of the application.

B. Sequence listing

The Examiner asked why the sequence listing entered on September 27, 2001 contained 324 sequences while the application as filed contained 6 sequences. The additional sequence numbers were added to represent the primers described on Figure 3 and the peptides encoded and listed in the reading frames under original SEQ ID NO:6 on pages 41-42. The additional numbers were added to conform with 37 CFR §§ 1.821-1.825, which requires a separate sequence number for each sequence described in the application. No new matter was added.

5. Claim objection

Claim 1 was objected to as allegedly lacking the phrase "that is." Although the meaning of the claims is the same whether or not that phrase is in the claim, to expedite prosecution, the phrase has been added. Applicants therefore respectfully request withdrawal of the objection.

6. Double Patenting Rejection

Claims 1, 2, 4-15 and 17-24 were rejected under the judicially-created doctrine of obviousness-type double patenting. Applicants will gladly address this issue when the claims have been indicated as otherwise allowable.

7. Rejection under 35 U.S.C. § 112, second paragraph

A. Claim 2

Claim 2 was rejected for reciting "at least about." Although the metes and bounds of the phrase is clear, to expedite prosecution, the word "about" is deleted. Accordingly, withdrawal of the rejection is respectfully requested.

B. Claims 9 and 15

Claims 9 and 15 were rejected for reciting "the polynucleotide of claim 1" because the phrase allegedly lacks antecedent basis. Line 2, of claim 1 refers to a "*FIE* polynucleotide" thereby providing antecedent basis for claims 9 and 15. For further clarification, claims 9 and 15 are amended to recite a "*FIE* polynucleotide." Therefore, withdrawal of the rejection is respectfully requested.

8. Rejection under 35 U.S.C. § 112, first paragraph

A. Written Description Rejection

Claims 1, 2, 5-7, 9, 10, 12, 13, 15, 18 and 20-24 were rejected under 35 U.S.C. § 112, first paragraph as containing subject matter not described in the specification so as to demonstrate possession of the invention. In particular, the Examiner asserted that the specification did not provide any description of functional domains of FIE. *See*, page 7, last paragraph of Office Action. Applicants respectfully traverse the rejection.

In contrast to the Examiner's assertion, the specification does in fact describe functional domains of FIE. Specifically, the specification indicates that FIE polypeptides comprise WD40 repeats. *See, e.g.*, page 4, lines 12-15, page 12, lines 26-27 and page 30, lines 16-18 of the specification. WD40 repeats are well known motifs that are involved in protein-protein interactions. As amended, claim 1 recites "[a]n isolated nucleic acid molecule comprising a *FIE* polynucleotide encoding a polypeptide at least 60% identical to SEQ ID NO:4, wherein the polypeptide comprises a WD40 repeat...." Thus, the claim specifically recites polypeptides having a particular structural domain.

Applicants submit that the Federal Circuit has held that the written description requirement can be fulfilled in any number of ways, so long as the specification describes the invention "in sufficient detail that one skilled in the art can clearly conclude that the inventor invented the claimed invention." *See University of California v. Eli Lilly & Co.*, 43 USPQ2d 1398, 1404 (Fed. Cir. 1997). For a chemical invention, an adequate description "requires a precise definition, such as by ***structure***,

formula, chemical name, or ***physical properties***...." (emphasis added). Accordingly, the present specification provides ample written description for the pending claims, precisely as required by the Court in *University of California*.

In the present case, amended claim 1 is directed to nucleic acid molecules comprising *FIE* polynucleotides encoding a polypeptide at least 60% identical to SEQ ID NO:4 wherein the polypeptide comprises a WD40 repeat and wherein the nucleic acid molecule enhances endosperm development in the absence of fertilization when the polynucleotide is operably linked to promoter to inhibit gene expression and introduced into a plant. The claims therefore provide at least two structural limitations: percent identity with a reference amino acid sequence and the presence of a well known protein motif. Thus, the specification defines a *physical* and *structural property* of the invention, as explicitly required by the court in *University of California*. Applicants therefore respectfully request withdrawal of the rejection.

Moreover, the claims only encompass polynucleotides with a particular function. As amended, the claims read polynucleotides that when linked to a promoter to inhibit gene expression and introduced in a plant results in enhanced endosperm development in the absence of fertilization.

In addition, Applicants note that new claim 29 is a method claim that includes the same hybridization conditions that were previously allowed in the parent application, now U.S. Patent No. 6,229,064. Accordingly, Applicants respectfully request withdrawal of the rejection.

B. Enablement Rejection

Claims 1, 2, 5-7, 9, 10, 12, 13, 15, 18 and 20-24 were rejected under 35 U.S.C. § 112, first paragraph as allegedly not enabled. According to the Examiner, methods of causing endosperm production in plants in the absence of fertilization using antisense molecules are enabled, but other methods of modulating endosperm development are not enabled. The Examiner suggested that Applicants amend the claims

to recite antisense methods of inducing endosperm development in the absence of fertilization. Applicants traverse the rejection.

As discussed above, the amended claims encompass polynucleotides encoding a polypeptide at least 60% identical to SEQ ID NO:4, wherein the polypeptide comprises a WD40 repeat and the polynucleotide enhances endosperm production in the absence of fertilization when the polynucleotide is linked to a promoter to inhibit gene expression and introduced into a plant. Those of skill in the art could have readily prepared and used polynucleotides within the full scope of the claim as of the filing date.

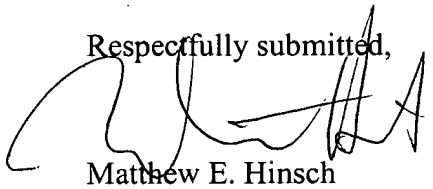
The Examiner correctly notes that inhibiting *FIE* gene expression results in increased endosperm production in the absence of fertilization. However, the Examiner is incorrect to assert that only antisense can be used to inhibit gene expression. The amended claims encompass both antisense and sense constructs. A number of methods for inhibiting gene expression were known and described in the application, including antisense and sense suppression (now commonly referred to as RNA interference). *See, e.g.*, pages 15-18 of the application. All of the methods of inhibiting gene expression described in the application are commonly used to affect gene expression in plants. Therefore, those of skill in the art were enabled to practice the full scope of the present claims, including sense and antisense constructs. Accordingly, Applicants respectfully request withdrawal of the rejection.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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APPENDIX A

VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Please amend the first paragraph on page 7 of the application as follows:

Another example of algorithm that is suitable for determining percent sequence identity and sequence similarity is the BLAST algorithm, which is described in Altschul *et al., J. Mol. Biol.* 215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information [(http://www.ncbi.nlm.nih.gov/)]. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al, supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a wordlength (W) of 11, the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

IN THE CLAIMS:

1. (Twice amended) An isolated [double-stranded] nucleic acid molecule comprising a *FIE* polynucleotide encoding a polypeptide at least 60% identical to SEQ ID NO:4, wherein the polypeptide comprises a WD40 repeat and wherein the nucleic acid molecule enhances endosperm development in the absence of fertilization when the polynucleotide is operably linked to promoter to inhibit gene expression and introduced into a plant.

2. (Twice amended) The isolated nucleic acid molecule of claim 1, wherein the *FIE* polynucleotide is at least [about] 100 nucleotides in length.

9. (Twice amended) A transgenic plant comprising an expression cassette containing a plant promoter operably linked to the *FIE* polynucleotide of claim 1, wherein the polynucleotide is heterologous to the plant promoter or the plant.

15. (Twice amended) A method of modulating endosperm development in a plant, the method comprising introducing into the plant an expression cassette containing a plant promoter operably linked to the *FIE* polynucleotide of claim 1, wherein the polynucleotide is heterologous to the plant promoter or the plant, and wherein introduction of the expression cassette into the plant inhibits gene expression.

25. (New) The method of claim 15, wherein the polynucleotide is at least 100 nucleotides in length.

26. (New) The method of claim 15, wherein the plant promoter is tissue-specific.

27. (New) The method of claim 15, wherein the plant promoter is ovule- or embryo-specific.

28. (New) The method of claim 15, wherein the polynucleotide is operably linked to the plant promoter in a sense orientation.

29. (New) The method of claim 15, wherein the polynucleotide specifically hybridizes to SEQ ID NO:3 in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, followed by one wash for 20 minutes in 0.2X SSC at a temperature of about 50°C.

APPENDIX B

CLAIMS PENDING UPON ENTRY OF AMENDMENT

1. (Twice amended) An isolated nucleic acid molecule comprising a *FIE* polynucleotide encoding a polypeptide at least 60% identical to SEQ ID NO:4, wherein the polypeptide comprises a WD40 repeat and wherein the nucleic acid molecule enhances endosperm development in the absence of fertilization when the polynucleotide is operably linked to promoter to inhibit gene expression and introduced into a plant.

2. (Twice amended) The isolated nucleic acid molecule of claim 1, wherein the *FIE* polynucleotide is at least 100 nucleotides in length.

5. The isolated nucleic acid molecule of claim 1, further comprising a plant promoter operably linked to the *FIE* polynucleotide.

6. The isolated nucleic acid molecule of claim 5, wherein the plant promoter is from a *FIE3* gene.

7. The isolated nucleic acid of claim 6, wherein the *FIE* polynucleotide is linked to the promoter in an antisense orientation.

8. The isolated nucleic acid molecule of claim 1, wherein the polypeptide is SEQ ID NO:4.

9. (Twice amended) A transgenic plant comprising an expression cassette containing a plant promoter operably linked to the *FIE* polynucleotide of claim 1, wherein the polynucleotide is heterologous to the plant promoter or the plant.

10. The transgenic plant of claim 9, wherein the heterologous *FIE* polynucleotide encodes a FIE polypeptide.

12. The transgenic plant of claim 9, wherein the heterologous *FIE* polynucleotide is linked to the promoter in an antisense orientation.

13. The transgenic plant of claim 9, wherein the plant promoter is from a *FIE* gene.

15. (Twice amended) A method of modulating endosperm development in a plant, the method comprising introducing into the plant an expression cassette containing a plant promoter operably linked to the *FIE* polynucleotide of claim 1, wherein the polynucleotide is heterologous to the plant promoter or the plant.

17. The method of claim 15, wherein the polypeptide has an amino acid sequence as shown in SEQ ID NO:4.

18. The method of claim 15, wherein the heterologous *FIE* polynucleotide is linked to the promoter in an antisense orientation.

19. The method of claim 15, wherein the heterologous *FIE* polynucleotide is SEQ ID NO:3.

20. The method of claim 15, wherein the plant promoter is from a *FIE* gene.

21. The method of claim 15, wherein the expression cassette is introduced into the plant through a sexual cross.

22. The isolated nucleic acid molecule of claim 1, wherein the polypeptide is at least 80% identical to SEQ ID NO:4.

23. The transgenic plant of claim 9, wherein the polypeptide is at least 80% identical to SEQ ID NO:4.

24. The method of claim 15, wherein the polypeptide is at least 80% identical to SEQ ID NO:4.

25. (New) The method of claim 15, wherein the polynucleotide is at least 100 nucleotides in length.

26. (New) The method of claim 15, wherein the plant promoter is tissue-specific.

27. (New) The method of claim 15, wherein the plant promoter is ovule- or embryo-specific.

28. (New) The method of claim 15, wherein the polynucleotide is operably linked to the plant promoter in a sense orientation.

29. (New) The method of claim 15, wherein the polynucleotide specifically hybridizes to SEQ ID NO:3 in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, followed by one wash for 20 minutes in 0.2X SSC at a temperature of about 50°C.